

-1-

SEQUENCE LISTING

<110> ICOS Corporation, et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC
INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810PCT

<140>

<141>

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

<213> Homo sapiens - human MDC cDNA

<220>

<221> CDS

<222> (20)..(298)

<220>

<221> mat_peptide

<222> (92)..(298)

<400> 1

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Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val

-20

-15

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100

Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr

-10

-5

-1 1

SUBSTITUTE SHEET (RULE 26)

-2-

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
 5 10 15

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
 20 25 30 35

tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc 244
 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
 40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
 55 60 65

agc caa tgaagagcct actctgatga ccgtggcctt ggctcctcca ggaaggctca 348
 Ser Gln

ggagccctac ctccctgcca ttatagctgc tccccgccag aagcctgtgc caactctctg 408
 cattccctga tctccatccc tgtggctgtc accctgggtc acctccgtgc tgtcactgcc 468
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 gttcccatca gcatctcccc tgcttaaacc ctcccatgac tccccactgc cctaagctga 588
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aggtaatccg cccacctcag cctcccaaag tgctgggatt acaggcgtga gccacagtgc 1488
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tgcccatgaa cggggcctc aagcgtcctg gcatctcctt cteccctctg tctgtcctt 2868
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<210> 2

<211> 93

<212> PRT

<213> Homo sapiens - human MDC

SUBSTITUTE SHEET (RULE 26)

-4-

<400> 2

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 3

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer JHSP6

<400> 3

gacactatag aatagggc

18

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer M13

<400> 4

gtaaaacgac ggccagt

17

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer T3.1

<400> 5

aattaaccct cactaaaggg

20

SUBSTITUTE SHEET (RULE 26)

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<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer T7.1

<400> 6
gtaatacgac tcactatagg gc

22

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-1F

<400> 7
tctatctaga ggcccctacg gcgccaacat ggaag

35

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-2R

<400> 8
caccggatcc tcattggctc agcttattga gaa

33

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-4R

<400> 9
aatggatcca cagcacggag gtgaccaag

29

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-3R

-6-

<400> 10
agtcaagctt agggcactct gggatcggca c

31

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-FX2

<400> 11
tatcggatcc tggttccgcy tggcccctac ggcgccaaca tggaa

45

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer GEX5

<400> 12
gaaatccagc aagtatatag ca

22

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-Pel

<400> 13
attgccatgg cggccccta cggcgccaac atggaa

36

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390RcH

<400> 14
gaccaagctt gagacataca ggacagagca

30

<210> 15
<211> 29
<212> DNA

SUBSTITUTE SHEET (RULE 26)

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tggatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgaaattaat acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
390mycRX

<400> 17

tggatctaga tcaattcaag tctctctgc tgatcagctt ctgctcttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<220>

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala

-20

-15

-10

Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr

-5

1

5

Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu

10

15

20

25

Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val

30

35

40

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-8-

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
60 65 70

Pro Lys Leu
75

<210> 19

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
-20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
-5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
45 50 55

80

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
60 65 70

Pro Lys Thr
75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<220>

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
50 55 60

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Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
 65 70 75

<210> 21

<211> 91

<212> PRT

<213> Homo sapiens - RANTES

<220>

<400> 21

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
 -20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
 -5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
 10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
 30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
 45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
 60 65

<210> 22

<211> 91

<212> PRT

<213> Homo sapiens - MIP-1 beta

<220>

<400> 22

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 -20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
 -15 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val
 10 15 20

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe
 30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp
 45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
 60 65

SUBSTITUTE SHEET (RULE 26)

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<210> 23
<211> 92
<212> PRT
<213> Homo sapiens - MIP-1 alpha

<220>
<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
-20 -15 -10
Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
-5 1 5 10
Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
15 20 25
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
30 35 40
Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
45 50 55
Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
60 65 70

<210> 24
<211> 96
<212> PRT
<213> Homo sapiens - I-309

<220>
<400> 24

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
-20 -15 -10
Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
-5 1 5
Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
10 15 20 25
Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe
30 35 40
Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
45 50 55
Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys
60 65 70

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<210> 25
 <211> 93
 <212> PRT
 <213> Artificial Sequence - Human MDC analog

<220>
 <223> The amino acid at position 24 is selected from the group consisting of arg, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
 <223> The amino acid at position 27 is independently selected from the group consisting of lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
 <223> The amino acid at position 30 is independently selected from the group consisting of tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>
 <223> The amino acid at position 50 is independently selected from the group consisting of glu, lys, arg, his, gly, and ala

<220>
 <223> The amino acid at position 59 is independently selected from the group consisting of trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>
 <223> The amino acid at position 60 is independently selected from the group consisting of val, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<400> 25
 Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
 -20 -15 -10
 Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
 -5 1 5
 Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa
 10 15 20
 Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 25 30 35 40

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Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 26

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-7F

<400> 26

tattggatcc gttctagctc cctgttctcc

30

<210> 27

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-8R

<400> 27

ccaagaattc ctgcagccac tttctgggct c

31

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA1

<400> 28

gcgactctct actgtttctc

20

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA2

<400> 29

cacaggaaac agctatgacc

20

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-13-

<210> 30
 <211> 70
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Human MDC analog
 <400> 30
 Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp
 1 5 10 15
 Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp
 20 25 30
 Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg
 35 40 45
 Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile
 50 55 60
 Leu Asn Lys Leu Ser Gln
 65 70

<210> 31
 <211> 69
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Human MDC analog
 <400> 31
 Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
 1 5 10 15
 Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr
 20 25 30
 Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
 35 40 45
 Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu
 50 55 60
 Asn Lys Leu Ser Gln
 65

<210> 32
 <211> 69
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Human MDC analog
 <400> 32

SUBSTITUTE SHEET (RULE 26)

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Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 33

<211> 1677

<212> DNA

<213> Homo sapiens - human CCR4 cDNA

<220>

<221> CDS

<222> (183)..(1262)

<400> 33

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tctctcattt cccttctcct tctccctcag tctccacatt caacattgac aagtccattc 120
agaaaagcaa gctgcttctg gttggggcca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
1 5 10 15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
20 25 30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
35 40 45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
50 55 60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
65 70 75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467
Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
80 85 90 95

SUBSTITUTE SHEET (RULE 26)

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| | |
|---|------|
| ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag | 515 |
| Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys | |
| 100 105 110 | |
| atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt | 563 |
| Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe | |
| 115 120 125 | |
| gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg | 611 |
| Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val | |
| 130 135 140 | |
| ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg | 659 |
| Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu | |
| 145 150 155 | |
| gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc | 707 |
| Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe | |
| 160 165 170 175 | |
| agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac | 755 |
| Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr | |
| 180 185 190 | |
| tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac | 803 |
| Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn | |
| 195 200 205 | |
| att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc | 851 |
| Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser | |
| 210 215 220 | |
| atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag | 899 |
| Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys | |
| 225 230 235 | |
| gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg | 947 |
| Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp | |
| 240 245 250 255 | |
| aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa | 995 |
| Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu | |
| 260 265 270 | |
| gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag | 1043 |
| Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln | |
| 275 280 285 | |
| gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc | 1091 |
| Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile | |
| 290 295 300 | |
| tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc | 1139 |
| Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe | |
| 305 310 315 | |

-16-

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187
 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu
 320 325 330 335

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc 1235
 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr
 340 345 350

atg gat cat gat ctt cat gat gct ctg taggaaaaat gaagatggtga 1282
 Met Asp His Asp Leu His Asp Ala Leu
 355 360

aatgcagagt caatgaactt ttccacattc agagcttact ttaaaattgg tatttttagg 1342

taagagatcc ctgagccagt gtcaggagga aggcttacac ccacagtga aagacagctt 1402

ctcactctgc aggcagcttt ttctctccca ctgacaaagt ccagcctggc aagggttcac 1462

ctgggctgag gcacccctcc tcacaccagg cttgcttgca ggcattgagc agtctgatga 1522

gaactctgag cagtgttga atgaagttgt aggtaattatt gcaaggcaaa gactattccc 1582

ttctaacctg aactgatggg ttctctccaga ggaattgca gactactggc tgatggagta 1642

aatcgctacc ttttgctgtg gcaaatgggc ccccg 1677

<210> 34

<211> 360

<212> PRT

<213> Homo sapiens - human CCR4

<400> 34

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
 1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
 20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
 50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
 85 90 95

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-17-

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
 100 105 110
 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
 115 120 125
 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 130 135 140
 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
 145 150 155 160
 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175
 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190
 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205
 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220
 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240
 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255
 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270
 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285
 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300
 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320
 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335
 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350
 Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 35

<211> 1784

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-18-

<212> DNA

<213> murine MDC cDNA

<220>

<221> CDS

<222> (1) .. (276)

<220>

<221> mat_peptide

<222> (73) .. (276)

<400> 35

atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct 48
 Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
 -20 -15 -10

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa 96
 Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
 -5 -1 1 5

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt 144
 Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
 10 15 20

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc 192
 Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
 25 30 35 40

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg 240
 Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
 45 50 55

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag 286
 Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
 60 65

gacctgatga ccatgggtct ggtgtggtcc agggaggctc agcaagccct attcttctgc 346

cattccagca agagccttgc caacgacgcc acctttactc acctccatcc cctgggctgt 406

cactctgtca ggctctgtgc cctctacctc cctctatcc cttccagctt atcccccttc 466

aatgtggcag ctgggaaaca cattcaggcc agccttacct aatgcctact cccactgct 526

ttagatgaga ccagcgtcct tgttttgatg cctgatcct atgatgcctt ccccatcccc 586

agccttggcc cctttctctt cttgcatgta gggaaggccc ataggtttca aatatgtgct 646

acctacttcc ctttctgggg ggttctaata cccagcatgt ttttctgct gcaggcacct 706

atccagtgcc acacacctcc caagtttcta tcagtcccag tgggcatcca ccaagcccca 766

aacttcagac ttccttggcc tccacctact cttagtagaa ttctgggagt ttcaggctgg 826

tccaccaggc ccccagggt taggccaagg tccccaccag agctcctcct gtttcttggt 886

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-19-

ctgcagcacg gggcagggag caaggagcag gctcagaatc agattttctta aaggagctgc 946
 agactccatc agtaaaagga atctttctcc catccctgaa tataaggcag ttttctgtca 1006
 acacagagac tcaggttggt agaaatggcc acatagatca actgtgaaac cctaaattta 1066
 ccaagaatca acttccaccc ctcttcaacc acatgctagg gtcttttact ttctctgccc 1126
 cacacctttg actccttgcc tgtgtagctg atagtcgaag ttatgctatg gtgtcagtga 1186
 ctgccacagt ttgtttggta ttataagcta tagttatatt tatataggaa agaggataaa 1246
 tatatgtggg ccaaatagac gaactggaga gttttaggat ctgggggcag gaagggccat 1306
 acaaagtgat acctcagaaa atagatgggt gtgggagctg ctgccagtgg cagagttaac 1366
 ttaaagaact taattgaaat tattcttgag tggctgaggg caagacaaga atatagaacc 1426
 cattcttgct tccttgagga caacagtggc cccaggggaa ggaataaacc ttcttgctcc 1486
 tctggaggga gcatggcctg rcttagccga gtgactggac tgtgtgagat tgggggcac 1546
 gcttttcty tctgagcctc agctgacagc atatgggacc acaaagggtc tgatccaaac 1606
 cacagggatt gacagtgcc gccacagctg tgtccagggc tcgtgttctg ccagaaggag 1666
 cacctggacg accagggcca ccactagtgc tactttgctc actgcccctg catgtcctga 1726
 aggtccctcc cctcctctc ctacttctgg gaaaataaat gctcgccaat aatacctg 1784

<210> 36

<211> 92

<212> PRT

<213> murine MDC

<400> 36

Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
 -20 -15 -10

Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
 -5 -1 1 5

Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
 10 15 20

Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
 25 30 35 40

Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
 45 50 55

Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
 60 65

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-20-

<210> 37
<211> 958
<212> DNA
<213> rat MDC cDNA

<220>
<221> CDS
<222> (1)..(243)

<220>
<221> mat_peptide
<222> (40)..(243)

<400> 37
ctc gtc ctt ctt gct gtg gca ctt cag acc tcc gat gca ggt ccc tat 48
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 -1 1
ggt gcc aat gtg gaa gac agt atc tgc tgc cag gac tac atc cgt cac 96
Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15
cct ctg cca cca cgt ttc gtg aag gag ttc tac tgg acc tca aag tcc 144
Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35
tgc cgc aag cct ggc gtc gtt ttg ata acc atc aag aac cga gat atc 192
Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50
tgt gct gac ccc ang atg ctc tgg gtg aag aag ata ctc cac aag ttg 240
Cys Ala Asp Pro Xaa Met Leu Thr Val Lys Lys Ile Leu His Lys Leu
55 60 65
gcc tagggagaag ggccctgatga ccacgggtct ggtgtctcca caaggctcag 293
Ala
caaaccctat ccttctgccca tccagcaaga gccttgccaa caactccacc ttgctcacc 353
tccatcccct gggttgtcac tctgtgaagc ctgggtccc tgtacttctt gtccgtcccc 413
tccagctcat tctcttccaa cgtggcagcc gggaagcact tctggctagc cttacccaat 473
actactcccc actgctttaa atgagaccag ggctcctgtt ttggtgcctt tggatcctat 533
gatgccttcc cagtctccag ccttggtccc cttctcttct tacatgtagg gaacaccaat 593
atctttcaag tatgtgtac ccaattcttc ttctcggag gctgctggga cccggaatat 653
tateccctgc tgcaggcttc tccaagcacc actcacctcc caggctttcc atccgtccca 713
gtcccaagcc ccattgttca gaacttcctt tggccccccc ctacactcca caaattctgg 773
ggaagtctca cnaactgggt cccctcaggc cccacggga aggaaggctc ccnccaaca 833

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-21-

acntcctect gttttccccg gtctcccncc nccgggantt gggcnccna atccccaaat 893
 tetgaanang aacngcccat tcntcccntt aaaattaacc tttccccccc tccctgagnt 953
 taggn 958

<210> 38
 <211> 81
 <212> PRT
 <213> rat

<400> 38
 Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
 -10 -5 -1 1
 Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
 5 10 15
 Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
 20 25 30 35
 Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
 40 45 50
 Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
 55 60 65

Ala

<210> 39
 <211> 506
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-pro/human MDC cDNA/chimeric construct

<221> CDS

<222> (15)..(476)

<220>

<221> mat_peptide

<222> (270)..(476)

<400> 39

atctcgagct cacg atg aga ttt cct tca att ttt act gca gtt tta ttc 50
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe
 -85 -80 -75

gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat 98
 Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp
 -70 -65 -60

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-22-

gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta 146
 Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu
 -55 -50 -45

gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat 194
 Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn
 -40 -35 -30

aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa 242
 Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys
 -25 -20 -15 -10

gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc gcc aac atg 290
 Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met
 -5 -1 1 5

gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg 338
 Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu
 10 15 20

cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct 386
 Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro
 25 30 35

ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc 434
 Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro
 40 45 50 55

aga gtg ccc tgg gtg aag atg att ctg aat aag ctg agc caa 476
 Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

tgaaggcctt ctagagcggc cgcacgcgata 506

<210> 40
 <211> 154
 <212> PRT
 <213> cDNA
 <400> 40

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75 -70

Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
 -50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -20 -15 -10

-23-

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val
 -5 -1 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys
 15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu
 30 35 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp
 45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

<210> 41

<211> 93

<212> PRT

<213> Artificial Human MDC analog

<220>

<223> The amino acid at position 2 is not proline

<220>

<400> 41

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
 -20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu
 -5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
 45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

<210> 42

<211> 538

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53) .. (334)

<220>

SUBSTITUTE SHEET (RULE 26)

-24-

<221> mat_peptide

<222> (122)..(334)

<400> 42

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ccctgagcag agggacctgc acacagagac tcctcctgg gctcctggca cc atg gcc 58
                                     Met Ala

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
   -20                -15                -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
   -5                -1    1                5                10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
           15                20                25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
           30                35                40

gtg cag ggc agg gcc atc tgt tgc gac ccc aac aac aag aga gtg aag 298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
           45                50                55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaagcctcc 344
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
           60                65                70

tcaccccgaga ctctgactg tctcccgga ctacctggga cctccaccgt tgggtgttcac 404

cgccccacc ctgagcgct ggggccagg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tcccatccc ttgtctgaac tggagccatg ggcacaaagg gccagatta 524

aagtctttat cctc 538

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<210> 43

<211> 94

<212> PRT

<213> Homo sapiens

<400> 43

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Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
           -20                -15                -10

Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
           -5                -1    1                5

Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
           10                15                20                25

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tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 291
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

-26-

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc
Ser Gln

335

<210> 46

<211> 93

<212> PRT

<213> Macaque MDC

<400> 46

Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala
-24 -20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

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